

What is claimed is:

1. A primer comprising the nucleotide sequence of SEQ ID NO: 1, which specifically amplifies *groEL2* gene fragment of *Streptomyces* species.

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2. A primer comprising the nucleotide sequence of SEQ ID NO: 2, which specifically amplifies *groEL2* gene fragment of *Streptomyces* species.

3. A polynucleotide comprising *groEL2* gene fragment derived from
10 *Streptomyces* species or fragment thereof, which is selected from the group consisting of the nucleotide sequences of SEQ ID NOs: 3 to 42.

4. A polynucleotide comprising *groEL2* gene fragment derived from a potato scab pathogenic microorganism or fragment thereof, which is selected
15 from the group consisting of the nucleotide sequences of SEQ ID NOs: 43 to 61.

5. A method for identifying *Streptomyces* species comprising the steps of

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- 1) amplifying *groEL2* gene fragment of target strain using a primer which is capable of specifically amplifying *groEL2* gene of *Streptomyces* species;
 - 2) analyzing the nucleotide sequence of *groEL2* gene fragment thus amplified; and
 - 3) comparing the nucleotide sequence obtained in Step 2) with
25 that of *groEL2* gene fragment of a reference strain.

6. The method of claim 5, wherein the primer is at least one selected from the group consisting of a primer comprising the nucleotide sequence of SEQ ID NO: 1 and a primer comprising the nucleotide sequence of SEQ ID NO: 2.

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7. The method of claim 5, wherein the *groEL2* gene fragment of a reference strain is selected from the group consisting of the nucleotide sequences of SEQ ID NOs: 3 to 42.

10 8. The method of claim 5, wherein the *groEL2* gene fragment of a reference strain is selected from the group consisting of the nucleotide sequences of SEQ ID NOs: 43 to 61.

15 9. The method of claim 5, wherein the step 3) further comprises the steps of comparing the nucleotide sequence of *groEL2* gene fragment of a target strain with that of a reference strain, multi-aligning the nucleotide sequences, and forming a phylogenetic tree.

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